

SEQUENCE LISTING

<110> DeBonte, Lorin R. Fan, Zhegong Miao, Guo-Hua

<120> FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF

<130> 07148-063003

<140> US 09/771,904

<141> 2001-01-29

<150> US 08/874,109

<151> 1997-06-12

<160> 70

<170> FastSEQ for Windows Version 4.0

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<211> 1155

<212> DNA

<213> Brassica napus

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<221> CDS

<222> (1) ... (1152)

<223> Wild type Fad2

<221> misc feature

<222> 205

<223> n = a, g, c, or t/u

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Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
20 25 30

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser

35

40

45

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser

50 55 60

tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

65					70					75					80	
		tac Tyr														288
		ggc Gly														336
		tac Tyr 115														384
		ctc Leu	_													432
		aac Asn														480
_	_	tca Ser	-													528
		acc Thr														576
		gcc Ala 195			_	_		_			_				_	624
_		ttc Phe				_					-	-		_		672
_		tac Tyr				_				_	_	_				720
	_	tac Tyr	-	-		_			_	_	_	_	_			768
	_	ccg Pro		_		_						_				816
_	_	cac His 275	_				_				_	_				864

Asp Trp Phe 290	agg gga Arg Gly		ı Ala									912
ttg aac aag Leu Asn Lys 305												960
ccg ttc tcc Pro Phe Ser		_				_	_	_		_		1008
ata aag ccg Ile Lys Pro	_				-							1056
gtt aag gcg Val Lys Ala 355				_	_	_				_	_	1104
gac agg caa Asp Arg Gln 370		_	Gly							_		1152
tga												1155
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<212> PRT	_		or Va	al								
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<212> PRT <213> Brassi <220> <223> Xaa = <400> 2 Met Gly Ala	Phe, Let Gly Gly 5	ı, Ile, Arg Met	: Gln	Val	10				_	15		
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His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165
                                    170
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                                185
            180
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
                            200
                                                 205
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
                                             220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                         235
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                                     250
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                                265
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
        275
                            280
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                        295
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305
                    310
                                         315
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
                                     330
                325
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
                                345
            340
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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                        375
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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act
                                                                       96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
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25

20

					aaa Lys											144
					tcc Ser											192
_					gcc Ala 70											240
				_	tgg Trp					_	_					288
		-	_		gtc Val		_		_	_				_		336
_	_		_		ctt Leu	_	_		-							384
			_		tac Tyr				_		_		_	_		432
					tcc Ser 150			_	-							480
_	_		_		aag Lys				_						-	528
	-			_	tta Leu	_	_	_						_	_	576
		-			gtc Val	_		_			-				_	624
_					aac Asn	_					_	_		_		672
_					gac Asp 230	_				_	_	_				720

ttc cgt '														768
gga gtc (Gly Val :	_	_		_						_				816
ttg cag (Leu Gln)	_				_				_	_				864
gat tgg Asp Trp 290														912
ttg aac a Leu Asn 1 305														960
ccg ttc f														1008
ata aag o	_	_					_		_		_	_		1056
gtt aag g Val Lys i														1104
gac agg (Asp Arg (370			_									_		1152
tga														1155
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1		5					10					15		
Glu Thr A	20					25	_				30			
Val Gly (35	гуѕ	пÀг	ATG	40	PIO	Pro	uis	cys	45	гÀг	Arg	ser	

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Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
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Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
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Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
                                105
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
                            120
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
                        135
                                            140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                                    170
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
            180
                                185
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
                            200
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
                                            220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                        235
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                245
                                    250
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                                265
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
                            280
                                                285
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                        295
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
                325
                                    330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
                                345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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                        375
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<211> 1155

<212> DNA

<213> Brassica napus

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<221> CDS

<222> (1)...(1152)

<223> Wild type Fad2

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							aca Thr			96
							tgt Cys			144
							atc Ile 60			192
_			_	_			ctc Leu			240
							tgc Cys			288
		 _		-			ggc Gly			336
_							ctc Leu			384
		_					agt Ser 140			432
							gtg Val			480
_	_	_		_			ctc Leu			528
							ctc Leu			576
							gac Asp			624

tgc cat ttc cac Cys His Phe His 210	_		
cag ata tac atc Gln Ile Tyr Ile 225		Gly Ile Leu A	
tac cgc tac gct Tyr Arg Tyr Ala			
gga gtt ccg ctt Gly Val Pro Leu 260			
ttg cag cac acg Leu Gln His Thr 275		_	
gat tgg ttg agg Asp Trp Leu Arg 290			 = -
ttg aac aag gtc Leu Asn Lys Val 305		Ile Thr Asp 7	
ctg ttc tcg acc Leu Phe Ser Thr			
ata aag ccg ata Ile Lys Pro Ile 340			
gtt aag gcg atg Val Lys Ala Met 355			
gac agg caa ggt Asp Arg Gln Gly 370			_
tga			1155
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<212> DNA

<213> Brassica napus

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aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg 528 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu gga ege ace gtg atg tta acg gtt eag tte act ete gge tgg eet ttg 576 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190

						tcg Ser									624
_						gct Ala 215					_	_			672
						gct Ala									720
	_		_	_	_	caa Gln		_	_	_	_	_	_		768
	_	_		_		gtc Val					_	_			816
_	_		_			tcc Ser									864
_		_			_	ttg Leu 295	-		_	_	_	_			912
_		_	_			aat Asn		_	_	_					960
_		_		_	_	cat His				_	-	_	_	_	 1008
	_	_		_		gag Glu			_	_			_	_	 1056
	_					gag Glu									1104
				-	-	aaa Lys 375		-						_	1152
tga															1155
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<213> Brassica napus

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gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg 35 40 45	
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala 50 55 60	
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His 65 70 75	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys 85 90 95	Val
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala 100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His 115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg 130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro 145 150 155	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro 165 170 175	Leu

						acg Thr										576
		_			_	tcg Ser										624
_						gct Ala 215					_	_	_	_		672
_					_	gct Ala				_	_	_				720
	_		_	_	_	caa Gln		_	_	_	_	_	_			768
	_			_		gtc Val					_	_				816
_	_		_			tcc Ser	_				_	_				864
_		_			_	ttg Leu 295	-		-	_		_				912
_		_	_			aat Asn		_	-	_						960
_		_		_	_	cat His				_	_	_	_	_		1008
						gag Glu										1056
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355 360 365 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu

380

375

370

145

150

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155

160

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	_			_		_	gtt Val	_								576
		_			_	_	999 Gly 200	_			_				_	624
_						_	ccc Pro				_	_		_		672
_							ggc Gly									720
	_		_	_	_		gga Gly									768
	_			_		_	aac Asn				_	_				816
_	_		_				ctg Leu 280				_	_				864
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							atc Ile									960
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315

310

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala

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ctc tcc tac ttc Leu Ser Tyr Phe	5 55			•
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_	_		_	cat His			_				_	_		 864
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	Phe		Leu	Val	Pro	Tyr		Ser	Trp	Lys	Tyr		His	Arg	Arg	His	
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	3		275	3	03	77 -	T	280 71a	ml- · ·	17. 7	7	7	285	m- · · · ·	03 -	T] -	
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_		acc act tac Thr Thr Tyr									
		cct ctc tac Pro Leu Tyr			_ -						
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		gac gac acc Asp Asp Thr 120									

ttc c Phe L 1		-						_					4	32
cat t His S 145							_	_	_				4	80
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gga c													5	76
tac t Tyr L	_	a Phe		_	_		-						6	24
tgc c Cys H 2													6	72
cag a Gln I 225				_	_				_	-	_		7:	20
ttc c	_												7	68
gga g Gly V		_	_		_						_		8	16
ttg c	-	s Thr				_				_	_		 8	64
gat to Asp T													9:	12
ttg a Leu A 305								-	_				91	60
ctg t													10	80

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Cys Phe Tyr Tyr V	al Ala Thr	Thr Tyr Phe		o His Pro 80							
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		_				Tyr 55				_				-		
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Cys 65	Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	Pro	His	Pro 80	
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cta																
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			_				tcc Ser		_		_					432
							gag Glu									480
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	_			_		_	gtt Val	-					 _	_		576
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_							ccc Pro									672
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Leu Thr	Glv	Val	85 Trn	Val	Tle	Δla	His	90 Glu	Cvs	Glv	His	His	95 Ala	Phe	
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Cys His		His	Pro	Asn	Ala		Ile	Tyr	Asn	Asp		Glu	Arg	Leu	
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Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Glu Ile
                       295
                                            300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
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                                        315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
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Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
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